

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Kathleen L. Horwath et al.

Examiner:

Serial No.: (not yet assigned)

Group No.:

Filed: June 7, 2001

Date: June 7, 2001

Title: NUCLEIC ACID SEQUENCES ENCODING TYPE III TENEBRIO
ANTIFREEZE PROTEINS AND METHOD FOR ASSAYING ACTIVITY

Assistant Commissioner for Patents
Washington, D.C. 20231

SUBMISSION OF "SEQUENCE LISTING"
AND COMPUTER READABLE COPY

Sir/Madame:

Submitted herewith are:

A. "Sequence Listings" for the nucleotide and/or amino acid sequences in this application, each "Sequence Listing" is assigned a separate identifier as required in 37 CFR Sections 1.821(c) and 37 CFR Sections 1.822 and 1.823;

B. A copy of each "Sequence Listing" submitted for this application in computer readable form in accordance with the requirements of 37 CFR Sections 1.821(e) and 1.824;

C. The following statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same as required in 37 CFR Section 1.821(f).

I hereby state that the information recorded in computer readable form is identical to the written sequence listing.

RB-125RI
PATENT

Respectfully submitted,

By: _____

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Binghamton, NY 13901

CERTIFICATE OF EXPRESS MAILING

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L.et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

(2) INFORMATION FOR SEQ. ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(ix) FEATURES:

- (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
 - (D) OTHER INFORMATION: Non-his-tagged, signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTGGATCAA AGAATTGGC ACGAGACTAC TAAG ATG AAG TTG CTC	36
Met Lys Leu Leu	
	-15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG	81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu	
-10	-5
	1

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT	126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys	
5	10
	15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC	171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg	
20	25
	30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT	216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe	
35	40
	45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG	261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val	
50	55
	60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC	306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn	
65	70
	75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA	351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg	
80	85
	90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG	396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met	
95	100
	105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCAAGA	439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *	
110	115

CTAGTAGATG GTTCAAATGG TGTGCTTAC ATATAAAAAT AAAGTGTTTC	489
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TGATGTAAAA AAAAAAAA AAAAAAAA AACTCGAGAG TATTCTAGAG	539
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CGGCCGCGGG CCCATCGTT TCCACCC	566
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(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Lys	Leu	Leu	Cys	Cys	Leu	Ile	Ser	Leu	Ile	Leu	Leu	Val	Thr	Val
-15															

Gln	Ala	Leu	Thr	Glu	Ala	Gln	Ile	Glu	Leu	Asn	Lys	Ile	Ser	Lys
1														

Lys	Cys	Gln	Asn	Glu	Ser	Gly	Val	Ser	Gln	Glu	Ile	Ile	Thr	Lys	Ala
15															

Arg	Asn	Gly	Asp	Trp	Glu	Asp	Asp	Pro	Lys	Leu	Lys	Arg	Gln	Val	Phe
35															

Cys	Val	Ala	Arg	Asn	Ala	Gly	Leu	Ala	Thr	Glu	Ser	Gly	Glu	Val	Val
50															

Val	Asp	Val	Leu	Arg	Glu	Lys	Val	Arg	Lys	Val	Thr	Asp	Asn	Asp	Glu
65															

Glu	Thr	Glu	Lys	Ile	Ile	Asn	Lys	Cys	Ala	Val	Lys	Arg	Asp	Thr	Val
80															

Glu	Glu	Thr	Val	Phe	Asn	Thr	Phe	Lys	Cys	Val	Met	Lys	Asn	Lys	Pro
95															

Lys	Phe	Ser	Pro	Val	Asp	*									
115															

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
 1 5 10 15

Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
 20 25 30

Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
 35 40 45

Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
 50 55 60

Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
 65 70 75 80

Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
 85 90 95

Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
 100 105 110

Ser Pro Val Asp *
 115

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(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC	46	
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316	
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val		
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361	
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr		
85	90	95
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406	
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro		
100	105	110
ATT GAT TAA TTGTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTAATA	455	
Ile Asp *		
115		
TCGTTATGTA AAAAAAAA AAAAAA	481	

(2) INFORMATION FOR SEQ. ID NO: 6

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2-3
- (ix) FEATURES
 - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46	
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	316	
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val		
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361	
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr		
85	90	95
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406	
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro		
100	105	110
ATT GAT TAA TTGTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA	455	
Ile Asp *		
115		
TCGTTATGAA AAAAAAAA AAAAAAA	482	

(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 8

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, and 7.5
- (ix) FEATURES
- (D) OTHER INFORMATION: Mature Protein for Tm 12.84
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys
1				5					10					15	
Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr
					20			25					30		
Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe
		35				40					45				
Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu
		50				55				60					
Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp
		65				70			75				80		
Lys	Ile	Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr
			85				90					95			
Ala	Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser
			100				105				110				
Pro	Ile	Asp	*												
		115													

(2) INFORMATION FOR SEQ. ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*

- (B) INDIVIDUAL/ISOLATE: none

- (C) CELL TYPE: fat body and whole organism

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA

- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46	
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316	
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val		
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361	
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr		
85	90	95
GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406	
Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro		
100	105	110
ATT GAT TAA TTGTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA	455	
Ile Asp *		
115		
TCGTTATGTA AAAAAAAA AAAAAA	481	

(2) INFORMATION FOR SEQ. ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL no

(iv) ANTI-SENSE: no

(vi) ANTI SENSE NO

(A) ORGANISM: *Tenebrio molitor*

(B) INERTIAL / ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

IMMEDIATE SOURCE:

(A) LIBRARY: C
(B) CLONE: B

(B) (2)
(iv) FEATURES

(a) OTHER INFORMATION: Precursor Protein for Clone 3-4

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 1 5 10 15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
 20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
 35 40 45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
 50 55 60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
 65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
 85 90 95

Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC Met Lys Leu Leu Cys Phe Ala Phe Ala Ala	46	
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	91	
-5	1	5
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser	136	
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	181	
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly	226	
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	271	
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	316	
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	361	
85	90	95
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	406	
100	105	110
ATT GAT TAA TTGTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA Ile Asp *	455	
115		
TCGTTATGAA AAAAAAAAAA AAAAAAAA	482	

(2) INFORMATION FOR SEQ. ID NO: 13

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
- (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Clone 3.9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90 95

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 14

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature protein for Clone 3.9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 1 5 10 15

Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
 20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
 35 40 45

Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
 50 55 60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
 65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
 85 90 95

Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
- (ix) FEATURES
 - (D) OTHER INFORMATION: Non-his-tagged, Signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC Met Lys Leu Leu Cys Phe Ala Phe Ala Ala	46	
-15	-10	
 ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	90	
-5	1	5
 AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	136	
10	15	20
 CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	181	
25	30	35
 CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	226	
40	45	50
 GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	271	
55	60	65
 AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	316	
70	75	80
 CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	361	
85	90	95
 GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	406	
100	105	110
 ATT GAT TAA TTGTTTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA Ile Asp *	455	
115		
 TCGTTATGTA AAAAAAAAAA AAAAAA	481	

(2) INFORMATION FOR SEQ. ID NO: 16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96
-55	-50
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
-45	-40
-35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	186
-30	-25
-20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	231
-15	-10
-5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276
1	5
10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	321
15	20
25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366
30	35
40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	411
45	50
55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456
60	65
70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501
75	80
85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	546
90	95
100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
105	110
115	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAA	645
AAAAAAACTCG AGCACCAACCA CCACCACAC TGAGAT	681

(2) INFORMATION FOR SEQ ID NO: 17

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

(2) INFORMATION FOR SEQ. ID NO: 18

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96	
Met Gly Ser Ser His His His His His His Ser		
-30	-25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141	
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-20	-15	-10
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186	
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln		
-5	1	5
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231	
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val		
10	15	20
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276	
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp		
25	30	35
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321	
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr		
40	45	50
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366	
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys		
55	60	65
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411	
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile		
70	75	80
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456	
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala		
85	90	95
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501	
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser		
100	105	110
CCT ATT GAT TAA CTCGAGCACCA ACCACCACCA CCACTGAGAT	543	
Pro Ile Asp *		
115		

(2) INFORMATION FOR SEQ. ID NO: 19

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
														-20	
														-30	
Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg
															-5
															-15
Gly	Ser	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys
															10
															1
Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val
															30
															25
Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu
															45
															35
Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn
															60
															55
Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu
															75
															65
Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu
															90
															80
Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp
															110
															95
Phe	Ser	Pro	Ile	Asp	*										
															115

(2) INFORMATION FOR SEQ. ID NO: 20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
- (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal Plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	186
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	231
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	321
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	411
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	546
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTACTA TC GTTATGAA AAAAAAAA	645
AAAAAAAAACTC GAGCACCAACC ACCACCACTGAGAT	682

(2) INFORMATION FOR SEQ. ID NO: 21

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
- (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

(2) INFORMATION FOR SEQ. ID NO: 22
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 543 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.3
 (ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, Signal minus
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -30 -25	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -20 -15 -10	141
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln -5 1 5	186
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val 10 15 20	231
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp 25 30 35	276
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr 40 45 50	321
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys 55 60 65	366
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile 70 75 80	411
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95	456
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110	501
CCT ATT GAT TAA CTCGAGCACCC ACCACCACCA CCACTGAGAT Pro Ile Asp * 115	543

(2) INFORMATION FOR SEQ. ID NO: 23

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
														-20	
														-25	
Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg
															-5
Gly	Ser	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys
1					5					10					
Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val
15					20					25					30
Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu
35										40					45
Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn
50										55					60
Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu
65										70					
Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu
80										85					90
Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp
95										100					110
Phe	Ser	Pro	Ile	Asp	*										
					115										

(2) INFORMATION FOR SEQ. ID NO: 24
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 13.17
(ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, Signal plus

TENEBRIO MOLITOR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -65 -60 -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -50 -45 -40	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser -20 -15 -10	231
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile -5 1 5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15 20	321
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	456
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu 70 75 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 90 95	546
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105 110	595
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG Phe Ser Pro Val Asp *	643
TGTGCTTTAC ATATAAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	693
TCCACCCCTC GAGCACCAACC ACCACCACTGAGAT	743
	777

(2) INFORMATION FOR SEQ. ID NO: 25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
 -25 -20 -15 -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
 -5 1 5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
 10 15 20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
 25 30 35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
 40 45 50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
 55 60 65 70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
 75 80 85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
 90 95 100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
 105 110 115

(2) INFORMATION FOR SEQ. ID NO: 26

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96	
-30	-25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141	
-20	-15	-10
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	186	
-5	1	5
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	231	
10	15	20
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	276	
25	30	35
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	321	
40	45	50
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	366	
55	60	65
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	411	
70	75	80
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	456	
85	90	95
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	501	
100	105	110
CCA GTT GAT TGA CTCGAGCACC ACCACCA CCAC TGAGAT Pro Val Asp *	543	
115		

(2) INFORMATION FOR SEQ. ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
 1 5 10 15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
 20 25 30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
 35 40 45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
 50 55 60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
 65 70 75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu
 80 85 90 95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
 100 105 110

Phe Ser Pro Val Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	9b
	-55 -50
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
	-45 -40 -35
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	186
	-30 -25 -20
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	231
	-15 -10 -5
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276
	1 5 10
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	321
	15 20 25
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366
	30 35 40
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	411
	45 50 55
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456
	60 65 70
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501
	75 80 85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val	546
	90 95 100
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
	105 110 115
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAA	645
AAAAAAACTCG AGCACCCACCA CCACCAACAC TGAGAT	681

(2) INFORMATION FOR SEQ. ID NO: 29

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
- (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

(2) INFORMATION FOR SEQ. ID NO: 30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
- (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His His His Ser	96
-30	-25
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
-20	-15
-10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	186
-5	1
5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	231
10	15
20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	276
25	30
35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	321
40	45
50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	366
55	60
65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	411
70	75
80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	456
85	90
95	
TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser	501
100	105
110	
CCT ATT GAT TAA CTCGAGCACCC ACCACCACCA CCACGTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 31

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96
	-55 -50
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
	-45 -40 -35
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	186
	-30 -25 -20
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	231
	-15 -10 -5
CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276
	1 5 10
AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp	321
	15 20 25
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366
	30 35 40
CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala	411
	45 50 55
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456
	60 65 70
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501
	75 80 85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	546
	90 95 100
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
	105 110 115
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAA	645
AAAAAAAACTC GAGCACCAACC ACCACCACTGAGAT	682

(2) INFORMATION FOR SEQ. ID NO: 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
-55												-45		

Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg
-40													-30		

Gly	Ser	Glu	Phe	Ala	Arg	Ala	Lys	Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala
-25													-15		

Phe	Ala	Ala	Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile
-10													5		

Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Glu	Ser	Gly	Val
10													20		

Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp
25													35		

Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Arg	Thr	Gly	Val
40													50		

Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	Lys	Leu
55													70		

Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val	Gln	Lys	Cys
75													85		

Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys
90													100		

Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Asp	Phe	Ser	Pro	Ile	Asp	*
105													115	

(2) INFORMATION FOR SEQ. ID NO: 34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fa

IMMEDIATE SOURCE:

(A) LIBRARY: cL

(B) CLOM

FEATURES **ADVERTISING** **CLASSIFIED ADVERTISING**

(D) OTHER INFORMATION: His-tagged.

TTCTTAACTGGG ATGCCATTCC CTGCTTACGGG ATAATTTTGT TTAGCTTAAC

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC
Met Gly Ser Ser His His His His His His Ser
-20 -25

```

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT      141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-20          -15          -10

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GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG 186
 Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln
 -5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG 231
 Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
 10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp
 25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT 321
 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr
 40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA
 Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
 55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC 411
 Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
 70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
 85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCCACCA CCACGTGAGAT
Pro Ile Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 36

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3b:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96
	-55 -50
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
	-45 -40 -35
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	186
	-30 -25 -20
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	231
	-15 -10 -5
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276
	1 5 10
AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	321
	15 20 25
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366
	30 35 40
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	411
	45 50 55
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456
	60 65 70
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501
	75 80 85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	546
	90 95 100
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
	105 110 115
TTTGGCTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAA	645
AAAAAAACTCG AGCACCCACCA CCACCAACAC TGAGAT	681

(2) INFORMATION FOR SEQ. ID NO: 37

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
- (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 115

(2) INFORMATION FOR SEQ. ID NO: 38

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
- (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96	
-30	-25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141	
-20	-15	-10
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	186	
-5	1	5
AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	231	
10	15	20
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	276	
25	30	35
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	321	
40	45	50
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	366	
55	60	65
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	411	
70	75	80
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	456	
85	90	95
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	501	
100	105	110
CCT ATT GAT TAA CTCGAGCACCA ACCACCACCA CCACTGAGAT	543	
Pro Ile Asp *		
115		

(2) INFORMATION FOR SEQ. ID NO: 39

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
- (ix) FEATURES
 - (D) OTHER INFORMATION: T_m 12.84 upper primer with Bam-H1 site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG

24

(2) INFORMATION FOR SEQ. ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Tm 12.84 lower primer with Xhol site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

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RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 42

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGGGATCCC TGACCGAGGC ACAA 24

(2) INFORMATION FOR SEQ. ID NO: 43

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Tm 13.17 lower primer with Xhol site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAACTGAGC TCGCC 25

(2) INFORMATION FOR SEQ. ID NO: 44

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
 - (D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCN TTC GCC GCC	46	
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAY GAA CAG ATA CAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
AGG AAC AAG ATC AGC AAA GAR TGC CAG CAG GNG TCC GGA GTG TCC	136	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAY GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG ARA ACT GGA	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAR GTG GAC AAG ATC GTG	316	
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val		
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361	
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr		
85	90	95
GAC ACC TTC AAG NNT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406	
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro		
100	105	110
ATT GAT TAA TTGTTTGTA TTTGRCTGAA TTTTGACAAT AAAGGTANTAA	455	
Ile Asp *		
115		
TCGTTATGNA AAAAAAAA AAAAAA	481	

(2) INFORMATION FOR SEQ. ID NO: 45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
 - (D) OTHER INFORMATION: Concensus of Seq ID #44 with Tm 13.17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY	46	
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN	136	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC	316	
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile		
70	75	80
RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN	361	
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala		
85	90	95
TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN	406	
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser		
100	105	110
CCN RTT GAT TRA NYNNYNNNA YTNGNNRNR NTTYRANAAT AAAGNNNNTN	458	
Pro Ile Asp *		
115		
TNRTNNNRNA AAAAAAAA AAAAAA	484	

(2) INFORMATION FOR SEQ. ID NO: 46

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
 - (D) OTHER INFORMATION: Concensus of Seq ID #45 with B1/B2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala -15	-10	46
NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5 1 5		91
NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser 10 15 20		136
NAA GAN RYN ATN RNN ARA GYY CGC ANN GGT GNC TNG GNN GAY GAY Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35		181
CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYY GRN Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50		226
NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60 65		271
AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile 70 75 80		316
NYN NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95		361
TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN ARN CCN RNN TYY TYN Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110		406
CNN RYT RNT TRN NYNNNNNNN YNNNGNNRNR NTTYRANAAT AAAGNNNYTN Pro Ile Asp * 115		458
TNRTNNNRNA AAAAAAAA AAAAAA		484

(2) INFORMATION FOR SEQ. ID NO: 47

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (vii) FEATURES
 - (D) OTHER INFORMATION: Concensus of Seq. ID #46 with AFP-3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGCNNRNNNN AAR ATG AAR YTN CTC YNN TGY YTN RYN YYY NYY RYY Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala -15	-10	46
NTN NTN RYC NNR RYY YAN GCY NTN ACY NAN RNA NNN NNN NAG NNR Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5 1 5		91
NNG NNY NAR NNC AGC RNN RNN TGY NAR NNN GNR NNY GGA GTR TCN Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser 10 15 20		136
NAA GAN NYN NTN RNN ARR GYY CGC ANN NGT GNN NNR GNN GAY GAY Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35		181
CCY AAA NTG AAR NNN CAN NYY YTY TGC NTN NYN ARG RNN NYY GRN Pro Lys Met Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50		226
NTN RYN RNN GNN NNN GGN GAN NYN NNN NYN GAN NNN NTN ARR RNN Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60 65		271
AAR NTN ANG NRN NNN NNN RNN RNN NNN RAR RAR RYN RRN RRN NTN Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile 70 75 80		316
NYN NNN ARN NNN NNN NNN NNG ARN RNN NYN NNN NAR NNN NNN NNN Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95		361
NNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN YCN NNN TNN NNN Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110		406
CNN NYN RNN TRN NNNNNNNNNN YNNRNNNNNN NNNNNNAAT AAANNNNNN Pro Ile Asp * 115		458
NNNNNNNNNA AAAAAAAA AAAAAA		484

(2) INFORMATION FOR SEQ. ID NO: 48

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE:
- (vii) FEATURES
- (viii) OTHER INFORMATION: General Concensus of Clones,
B1, B2 and AFP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala			
Cys	Leu Ile Ser Leu Ile Leu Leu Val Thr Val		
	Thr Leu Val		Ala Ala Thr
	Val		
-15	-10		-5
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys			
Tyr Ile Glu Ala Asp Leu Glu Leu Leu Arg Gln Thr Ala			
	Thr Pro Arg	Lys His	Asp
1	5	10	
Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val			
Lys Lys Asn Val	Ala	Glu Asp Ile Leu Thr Arg Ala	
Ala Thr		Ala Val Lys	
	Ala	Ser Asn	
15	20	25	30
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu			
Asn Arg Asp Trp Glu		Leu Arg Gln Leu Phe	
Lys Glu Glu		Met Ala	
		Glu	
35	40	45	
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn			
Val Ala Arg Arg Ala Ile Leu Val Ala Ala Ser		Glu Ile Glu	
Ile Phe Ala Leu Glu Ile Ile Asp		Val Val	
Leu Asn Glu		Phe Gln	
50	55	60	
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser ^^^ Asp Glu			
Ala Asp Thr Phe Arg Glu	Val Thr Arg Asn Thr Asn Asp Pro		
Leu His Ile Thr	Phe Arg Lys Ser Asp Asn		
	Glu	Glu His	
65	70	75	
Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro			
Lys Ser Glu Asp Leu Ile Glu	Ala	Thr Glu Asp	Val
Thr Asn	Thr	Arg	
	Ala		
80	85	90	
Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro			
Gln Asp Ser Val Phe Glu Val Thr	Val Val Leu Lys Asn Arg Ser		
His Ser Ala Asn Phe	Met Asp		
	His		
95	100	105	110
Asp Phe Ser Pro Ile Asp ^^^ ^^^ *			
Asn Phe Gly Asp Leu Phe Val *			
Lys Val	*		
	115		